



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/724,264
Source: 1FW0
Date Processed by STIC: 12/19/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 10/08/03



RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/724,264

DATE: 12/19/2003

TIME: 13:02:10

Input Set : A:\02716.0005.NPUS01.ST25.txt
 Output Set: N:\CRF4\12192003\J724264.raw

3 <110> APPLICANT: JENSEN, Rasmus B.
 4 KELEMEN, Bradley
 6 <120> TITLE OF INVENTION: PROTEORHODOPSIN MUTANTS WITH IMPROVED OPTICAL CHARACTERISTICS
 8 <130> FILE REFERENCE: 02716.0005.NPUS01
 > 10 <140> CURRENT APPLICATION NUMBER: US/10/724,264
 > 10 <141> CURRENT FILING DATE: 2003-11-26
 10 <150> PRIOR APPLICATION NUMBER: 60/429,518
 11 <151> PRIOR FILING DATE: 2002-11-26
 13 <160> NUMBER OF SEQ ID NOS: 212
 15 <170> SOFTWARE: PatentIn version 3.2
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 18 <211> LENGTH: 252
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Marine eubacteria
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 28 Ser Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly
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 32 Val Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe
 33 35 40 45
 36 Phe Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu
 37 50 55 60
 40 Ala Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr
 41 65 70 75 80
 44 Met Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg
 45 85 90 95
 48 Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr
 49 100 105 110
 52 Leu Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys
 53 115 120 125
 56 Leu Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu
 57 130 135 140
 60 Ala Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly
 61 145 150 155 160
 64 Trp Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala
 65 165 170 175
 68 Val Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met
 69 180 185 190
 72 Met Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala
 73 195 200 205
 76 Gly Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu
 77 210 215 220

pp 6-7
 Does Not Comply
 Corrected Discette Needed

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 85 245 250
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 90 <212> TYPE: DNA
 91 <213> ORGANISM: Marine eubacteria
 93 <400> SEQUENCE: 2

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 96 gctggtggcg atctagatata aagtgatact gttgggtttt cattctggct ggttacagct 120
 98 ggtatgttag cggcaactgt gttctttttt gtagaaagag accaagttag cgctaagtgg 180
 100 aaaacttac ttgctgtatc tggtttaattt actggatatac ctttttggca ttatcttat 240
 102 atgagaggtg tttggataga cactgggtat accccaaacag tattcagata tattgattgg 300
 104 ttattaaactg ttccattaca aatgggttagt ttctatctaa ttcttgctgc ttgtacaagt 360
 106 gttgctgctt cattattaa gaagcttcta gctgggttcat tagtaatgtt aggtgctgga 420
 108 tttgcaggcg aagctggatt agctcctgtt ttacctgtt tcattattgg tatggctgga 480
 110 tggttataca tgatttatga gctatatacg ggtgaaggta aggctgtgt aagtactgca 540
 112 agtcctgctg ttaactctgc atacaacgc atgatgatga ttattgttgg tggatgggca 600
 114 atttacccgt ctggatatgc tgctggttac ctaatgggtg gcgaaagggtg atacgcttca 660
 116 aacttaaacc ttatataaa ccttgcgc ac cttgttaca agattctatt tgggttgc 720
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121 <210> SEQ ID NO: 3
 122 <211> LENGTH: 249
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 124 <213> ORGANISM: Marine eubacteria
 126 <400> SEQUENCE: 3

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 132 Ala Ala Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val Ser
 133 20 25 30
 136 Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe Phe
 137 35 40 45
 140 Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val
 141 50 55 60
 144 Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg
 145 65 70 75 80
 148 Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile
 149 85 90 95
 152 Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile
 153 100 105 110
 156 Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu Leu
 157 115 120 125
 160 Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly
 161 130 135 140
 164 Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp Val
 165 145 150 155 160
 168 Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys Asn
 169 165 170 175

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Input Set : A:\02716.0005.NPUS01.ST25.txt

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172 Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile
 173 180 185 190
 176 Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr
 177 195 200 205
 180 Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr Asn
 181 210 215 220
 184 Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn
 185 225 230 235 240
 188 Val Ala Val Lys Glu Ser Ser Asn Ala
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 200 ggtgaccttg atgcttagtga ttacactgggt gtttctttt ggttagttac tgctgcctta 120
 202 ttagcatcta ctgtatttt ctttggaa agagatagag tttctgcaaa atggaaaaca 180
 204 tcattaactg tatctggct tttactgggtt attgctttct ggcattacat gtacatgaga 240
 206 ggggtatggaa ttgaaactgg tgattcgcca actgtattta gatacattga ttggttacta 300
 208 acagttccctc tattaatatg tgaattctac ttaattcttgc ctgctgcaac taatgttgct 360
 210 ggatcattat ttaagaaatt actagttgtt tctcttggta tgcttgggtt tggttacatg 420
 212 ggtgaagcag gaatcatggc tgcattggcgc gcattcatta ttgggtgtt agcttggta 480
 214 tacatgattt atgaattatg ggctggagaa ggaaaatctg catgtataac tgcaagtcc 540
 216 gctgtgcaat cagcttacaa cacaatgtatg tatattatca tcttgggttgc ggcgatttat 600
 218 cctgttaggtt attcacagg ttacctgtatg ggtgacgggtg gatcagctct taacttaaac 660
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 236 Thr Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly
 237 20 25 30
 240 Val Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe
 241 35 40 45
 244 Phe Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu
 245 50 55 60
 248 Thr Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr
 249 65 70 75 80
 252 Met Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg
 253 85 90 95
 256 Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr
 257 100 105 110
 260 Leu Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys
 261 115 120 125

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Input Set : A:\02716.0005.NPUS01.ST25.txt

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264 Leu Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu
 265 130 135 140
 268 Ala Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala
 269 145 150 155 160
 272 Trp Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala
 273 165 170 175
 276 Cys Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met
 277 180 185 190
 280 Tyr Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr
 281 195 200 205
 284 Gly Tyr Leu Met Gly Asp Gly Ser Ala Leu Asn Leu Asn Leu Ile
 285 210 215 220
 288 Tyr Asp Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 289 225 230 235 240
 292 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala Lys
 293 245 250
 296 <210> SEQ ID NO: 6
 297 <211> LENGTH: 252
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 299 <213> ORGANISM: Marine eubacteria
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 304 1 5 10 15
 307 Thr Phe Ala Ala Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly
 308 20 25 30
 311 Val Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe
 312 35 40 45
 315 Phe Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu
 316 50 55 60
 319 Thr Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr
 320 65 70 75 80
 323 Met Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg
 324 85 90 95
 327 Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr
 328 100 105 110
 331 Leu Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys
 332 115 120 125
 335 Leu Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu
 336 130 135 140
 339 Ala Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala
 340 145 150 155 160
 343 Trp Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala
 344 165 170 175
 347 Cys Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met
 348 180 185 190
 351 Tyr Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr
 352 195 200 205
 355 Gly Tyr Leu Met Gly Asp Gly Ser Ala Leu Asn Leu Asn Leu Ile
 356 210 215 220

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359 Tyr Asp Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 360 225 230 235 240
 363 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala Lys
 364 245 250
 367 <210> SEQ ID NO: 7
 368 <211> LENGTH: 252
 369 <212> TYPE: PRT
 370 <213> ORGANISM: Marine eubacteria
 372 <400> SEQUENCE: 7

374 Thr Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro
 375 1 5 10 15
 378 Thr Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly
 379 20 25 30
 382 Val Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe
 383 35 40 45
 386 Phe Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu
 387 50 55 60
 390 Thr Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr
 391 65 70 75 80
 394 Met Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg
 395 85 90 95
 398 Tyr Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr
 399 100 105 110
 402 Leu Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys
 403 115 120 125
 406 Leu Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu
 407 130 135 140
 410 Ala Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala
 411 145 150 155 160
 414 Trp Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala
 415 165 170 175
 418 Cys Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met
 419 180 185 190
 422 Ala Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Ile Gly Tyr Phe Thr
 423 195 200 205
 426 Gly Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile
 427 210 215 220
 430 Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 431 225 230 235 240
 434 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala Lys
 435 245 250
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 441 <213> ORGANISM: Marine eubacteria
 443 <400> SEQUENCE: 8

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 446 ggtggcggtg accttgatgc tagtgattac actgggtttt ctttttgggtt agttacagct 120
 448 gctctattag catctactgt attttcttt gttgaaagag atagagttc tgcaaaatgg 180

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\02716.0005.NPUS01.ST25.txt
Output Set: N:\CRF4\12192003\J724264.raw

of <220> Feature(NEW RULES):
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of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
Unknown". Please explain source of genetic material in <220> to <223>
tion (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
c.1.823 of new Rules)

#:186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203
#:204,205,212

(see p. 7 for samples)

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7

<210> SEQ ID NO 186

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<212> TYPE: DNA

<213> ORGANISM: *artificial sequence*

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<400> SEQUENCE: 186

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24

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<220> FEATURE:

<223> OTHER INFORMATION: *Explanation needed*

<400> SEQUENCE: 187

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21

VERIFICATION SUMMARY

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Output Set: N:\CRF4\12192003\J724264.raw

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0 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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